Full wwPDB X-ray Structure Validation Report

Jan 31, 2016 – 09:09 PM GMT

PDB ID	:	1NQE
Title	:	OUTER MEMBRANE COBALAMIN TRANSPORTER (BTUB) FROM E. COLI
Authors	:	Chimento, D.P.; Mohanty, A.K.; Kadner, R.J.; Wiener, M.C.
Deposited on	:	2003-01-21
Resolution	:	2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

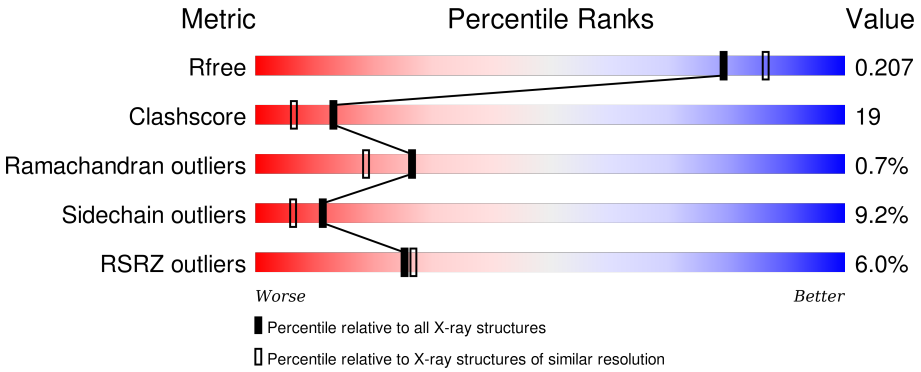
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	594	6% 69% 18% 5% • 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	C8E	A	800	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	C8E	A	801	-	-	-	X
3	C8E	A	802	-	-	-	X
3	C8E	A	803	-	-	X	X
3	C8E	A	805	-	-	X	X
3	C8E	A	806	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4733 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

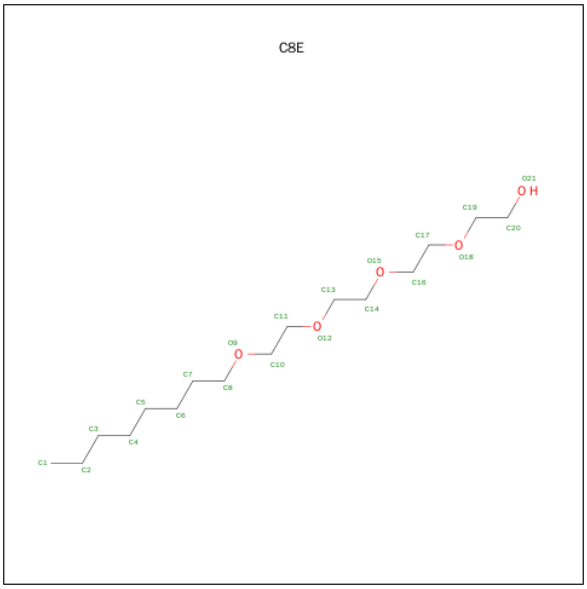
- Molecule 1 is a protein called Vitamin B12 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	549	Total	C	N	O	S	0	0	0
			4350	2742	748	858	2			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: $C_{16}H_{34}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			21	16	5		
3	A	1	Total	C	O	0	0
			21	16	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			21	16	5		
3	A	1	Total	C	O	0	0
			21	16	5		
3	A	1	Total	C	O	0	0
			21	16	5		
3	A	1	Total	C	O	0	0
			21	16	5		
3	A	1	Total	C	O	0	0
			21	16	5		

- Molecule 4 is water.

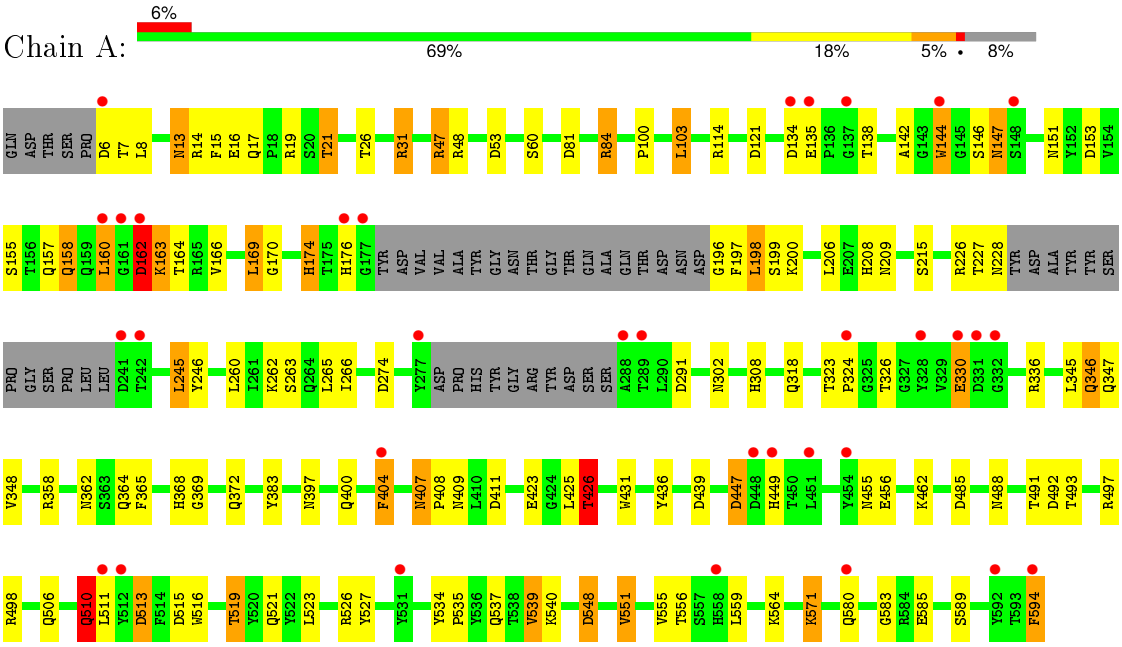
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	235	Total	O	0	0
			235	235		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Vitamin B12 receptor

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	81.59Å 81.59Å 210.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.92 – 2.00 24.87 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (24.92-2.00) 99.6 (24.87-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.194 , 0.232 0.207 , 0.207	Depositor DCC
R_{free} test set	2818 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	37.4	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 62.3	EDS
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 55457 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4733	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, C8E

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.85	6/4455 (0.1%)	0.97	21/6059 (0.3%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	510	GLN	CD-NE2	10.38	1.58	1.32
1	A	571	LYS	CE-NZ	9.21	1.72	1.49
1	A	571	LYS	CD-CE	7.90	1.71	1.51
1	A	537	GLN	CD-OE1	6.34	1.37	1.24
1	A	226	ARG	CG-CD	5.18	1.64	1.51
1	A	426	THR	CB-CG2	-5.01	1.35	1.52

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	537	GLN	OE1-CD-NE2	-8.74	101.80	121.90
1	A	498	ARG	NE-CZ-NH2	-7.77	116.42	120.30
1	A	134	ASP	CB-CG-OD2	7.02	124.62	118.30
1	A	515	ASP	CB-CG-OD2	6.63	124.26	118.30
1	A	497	ARG	NE-CZ-NH2	-6.37	117.12	120.30
1	A	162	ASP	CB-CG-OD2	6.04	123.74	118.30
1	A	513	ASP	CB-CG-OD2	5.92	123.62	118.30
1	A	548	ASP	CB-CG-OD2	5.87	123.58	118.30
1	A	81	ASP	CB-CG-OD2	5.73	123.45	118.30
1	A	447	ASP	CB-CG-OD2	5.66	123.39	118.30
1	A	84	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	A	439	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	492	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	485	ASP	CB-CG-OD2	5.52	123.27	118.30
1	A	274	ASP	CB-CG-OD2	5.50	123.25	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	497	ARG	NE-CZ-NH1	5.30	122.95	120.30
1	A	153	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	571	LYS	CD-CE-NZ	-5.21	99.70	111.70
1	A	84	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	A	53	ASP	CB-CG-OD2	5.04	122.83	118.30
1	A	6	ASP	CB-CG-OD2	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4350	0	4109	141	0
2	A	1	0	0	0	0
3	A	147	0	238	35	0
4	A	235	0	0	10	0
All	All	4733	0	4347	167	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (167) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:LYS:NZ	1:A:571:LYS:CE	1.72	1.49
3:A:802:C8E:H52	3:A:802:C8E:C1	1.49	1.31
1:A:169:LEU:HD13	1:A:170:GLY:N	1.67	1.09
3:A:802:C8E:C5	3:A:802:C8E:H13	1.79	1.09
1:A:169:LEU:C	1:A:169:LEU:HD13	1.75	1.04
3:A:802:C8E:H52	3:A:802:C8E:H13	0.97	0.96
3:A:802:C8E:C5	3:A:802:C8E:C1	2.40	0.96
3:A:803:C8E:H13	3:A:805:C8E:C14	1.97	0.95
1:A:198:LEU:HD13	1:A:199:SER:N	1.82	0.94
1:A:169:LEU:C	1:A:169:LEU:CD1	2.37	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:ARG:HH12	1:A:519:THR:HG21	1.37	0.90
1:A:197:PHE:HD2	1:A:227:THR:HG22	1.35	0.90
1:A:197:PHE:CD2	1:A:227:THR:HG22	2.08	0.88
1:A:411:ASP:H	1:A:455:ASN:HD21	1.18	0.88
3:A:802:C8E:H52	3:A:802:C8E:H12	1.57	0.87
1:A:527:TYR:CE1	1:A:540:LYS:HG3	2.10	0.87
1:A:160:LEU:HD23	1:A:166:VAL:HG21	1.55	0.86
1:A:516:TRP:CE3	1:A:551:VAL:HG13	2.11	0.85
1:A:506:GLN:HE22	1:A:519:THR:CG2	1.91	0.83
1:A:198:LEU:HD13	1:A:198:LEU:C	2.00	0.81
3:A:803:C8E:H13	3:A:805:C8E:H141	1.62	0.80
1:A:169:LEU:HD13	1:A:170:GLY:CA	2.12	0.78
1:A:135:GLU:H	1:A:157:GLN:HE22	1.32	0.78
1:A:539:VAL:CG2	1:A:540:LYS:N	2.48	0.77
1:A:580:GLN:HG2	4:A:953:HOH:O	1.83	0.77
1:A:426:THR:CG2	1:A:431:TRP:HE1	1.96	0.77
1:A:198:LEU:C	1:A:198:LEU:CD1	2.53	0.76
1:A:144:TRP:C	1:A:144:TRP:CD1	2.61	0.73
1:A:404:PHE:O	1:A:404:PHE:HD2	1.71	0.73
1:A:539:VAL:HG22	1:A:540:LYS:N	2.01	0.73
1:A:397:ASN:H	1:A:400:GLN:HE21	1.37	0.72
1:A:506:GLN:NE2	1:A:519:THR:HB	2.04	0.72
1:A:160:LEU:HD23	1:A:166:VAL:CG2	2.19	0.72
1:A:146:SER:O	1:A:147:ASN:HB2	1.88	0.72
1:A:100:PRO:HG2	1:A:103:LEU:HD22	1.71	0.71
1:A:358:ARG:O	3:A:800:C8E:H82	1.90	0.71
1:A:506:GLN:HE22	1:A:519:THR:HG22	1.55	0.71
1:A:362:ASN:ND2	1:A:364:GLN:H	1.89	0.70
1:A:47:ARG:NH2	4:A:832:HOH:O	2.25	0.70
3:A:803:C8E:C1	3:A:805:C8E:C14	2.71	0.69
1:A:397:ASN:H	1:A:400:GLN:NE2	1.92	0.68
1:A:48:ARG:NH1	1:A:519:THR:HG21	2.10	0.66
1:A:516:TRP:CE3	1:A:551:VAL:CG1	2.78	0.66
3:A:803:C8E:H112	3:A:805:C8E:H82	1.78	0.66
1:A:534:TYR:CG	1:A:535:PRO:HA	2.30	0.66
1:A:369:GLY:C	3:A:800:C8E:H111	2.16	0.66
1:A:13:ASN:ND2	1:A:15:PHE:H	1.95	0.65
3:A:803:C8E:H13	3:A:805:C8E:O15	1.96	0.65
1:A:174:HIS:CE1	1:A:176:HIS:CE1	2.85	0.64
1:A:383:TYR:OH	1:A:426:THR:HB	1.98	0.64
1:A:407:ASN:C	1:A:407:ASN:HD22	2.00	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:TRP:HD1	1:A:144:TRP:C	2.02	0.63
1:A:571:LYS:CD	1:A:571:LYS:NZ	2.62	0.63
1:A:491:THR:HG23	1:A:493:THR:H	1.63	0.63
1:A:411:ASP:H	1:A:455:ASN:ND2	1.93	0.63
1:A:516:TRP:CZ3	1:A:551:VAL:HG13	2.33	0.62
1:A:114:ARG:HA	1:A:372:GLN:HE22	1.64	0.62
1:A:144:TRP:HD1	1:A:144:TRP:O	1.83	0.61
1:A:47:ARG:NH2	1:A:548:ASP:OD2	2.26	0.61
3:A:802:C8E:H101	3:A:802:C8E:H141	1.82	0.60
1:A:491:THR:CG2	1:A:493:THR:OG1	2.50	0.60
3:A:803:C8E:C1	3:A:805:C8E:H141	2.31	0.59
1:A:19:ARG:HE	1:A:26:THR:HG23	1.68	0.59
1:A:539:VAL:CG2	1:A:540:LYS:H	2.16	0.58
1:A:323:THR:HG23	1:A:324:PRO:HD2	1.85	0.58
1:A:135:GLU:H	1:A:157:GLN:NE2	1.98	0.58
1:A:527:TYR:CZ	1:A:540:LYS:HG3	2.37	0.58
1:A:510:GLN:NE2	4:A:902:HOH:O	2.37	0.58
1:A:488:ASN:CG	1:A:491:THR:HG22	2.25	0.57
1:A:426:THR:HG23	1:A:431:TRP:HE1	1.70	0.57
1:A:19:ARG:HE	1:A:26:THR:CG2	2.18	0.56
1:A:516:TRP:CZ3	1:A:551:VAL:CG1	2.88	0.56
1:A:174:HIS:C	1:A:174:HIS:CD2	2.77	0.56
1:A:539:VAL:HG23	1:A:540:LYS:H	1.70	0.56
1:A:245:LEU:HD23	1:A:246:TYR:N	2.22	0.55
1:A:358:ARG:O	3:A:800:C8E:C8	2.54	0.55
1:A:245:LEU:CD2	1:A:246:TYR:N	2.69	0.55
1:A:174:HIS:HE1	1:A:176:HIS:CE1	2.25	0.55
3:A:803:C8E:C11	3:A:805:C8E:H61	2.37	0.54
1:A:426:THR:HG22	1:A:431:TRP:HE1	1.73	0.54
1:A:13:ASN:HD22	1:A:15:PHE:H	1.54	0.54
1:A:362:ASN:HD22	1:A:365:PHE:H	1.56	0.54
1:A:13:ASN:HD22	1:A:13:ASN:C	2.10	0.54
1:A:534:TYR:CD2	1:A:535:PRO:HA	2.42	0.54
1:A:447:ASP:OD2	1:A:449:HIS:HB2	2.07	0.54
1:A:510:GLN:N	1:A:510:GLN:NE2	2.56	0.54
1:A:336:ARG:HD3	4:A:1010:HOH:O	2.08	0.54
1:A:407:ASN:ND2	1:A:409:ASN:H	2.07	0.53
1:A:491:THR:HG23	1:A:493:THR:OG1	2.09	0.53
1:A:506:GLN:NE2	1:A:519:THR:CB	2.72	0.53
1:A:368:HIS:HD2	4:A:957:HOH:O	1.92	0.52
1:A:358:ARG:C	3:A:800:C8E:H71	2.30	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LEU:CD2	1:A:166:VAL:HG21	2.34	0.52
1:A:263:SER:OG	1:A:302:ASN:ND2	2.42	0.52
1:A:198:LEU:HD11	1:A:200:LYS:HG3	1.92	0.52
1:A:521:GLN:HE21	1:A:523:LEU:HD21	1.75	0.51
1:A:491:THR:HG21	1:A:493:THR:OG1	2.11	0.51
1:A:462:LYS:HB3	3:A:804:C8E:H172	1.92	0.51
1:A:135:GLU:OE1	1:A:135:GLU:HA	2.10	0.50
1:A:527:TYR:CE1	1:A:540:LYS:CG	2.90	0.50
1:A:245:LEU:C	1:A:245:LEU:CD2	2.79	0.50
1:A:407:ASN:C	1:A:407:ASN:ND2	2.65	0.49
1:A:13:ASN:O	1:A:14:ARG:HB2	2.12	0.49
1:A:368:HIS:HE1	4:A:847:HOH:O	1.95	0.49
1:A:169:LEU:O	1:A:169:LEU:CD1	2.61	0.49
1:A:174:HIS:HB2	1:A:198:LEU:HD22	1.95	0.48
3:A:803:C8E:H82	3:A:806:C8E:H22	1.96	0.48
1:A:583:GLY:O	1:A:585:GLU:HG3	2.14	0.48
1:A:407:ASN:HD22	1:A:409:ASN:H	1.60	0.48
1:A:488:ASN:HB3	1:A:491:THR:HG22	1.96	0.48
1:A:404:PHE:CD2	1:A:404:PHE:O	2.58	0.47
1:A:196:GLY:N	1:A:228:ASN:HD22	2.12	0.47
1:A:519:THR:HG23	4:A:872:HOH:O	2.15	0.47
1:A:516:TRP:CD2	1:A:551:VAL:CG1	2.98	0.47
1:A:346:GLN:NE2	3:A:805:C8E:H202	2.30	0.47
1:A:519:THR:CG2	4:A:872:HOH:O	2.63	0.46
1:A:506:GLN:HE22	1:A:519:THR:CB	2.27	0.46
1:A:506:GLN:NE2	1:A:519:THR:CG2	2.70	0.46
3:A:803:C8E:H111	3:A:805:C8E:H61	1.97	0.46
1:A:17:GLN:OE1	1:A:21:THR:HG22	2.15	0.46
1:A:13:ASN:ND2	1:A:13:ASN:C	2.69	0.45
1:A:144:TRP:CD1	1:A:144:TRP:O	2.65	0.45
1:A:404:PHE:C	1:A:404:PHE:CD2	2.89	0.45
1:A:8:LEU:HD13	1:A:16:GLU:OE2	2.16	0.45
1:A:516:TRP:CH2	1:A:551:VAL:HG11	2.52	0.45
3:A:802:C8E:C14	3:A:802:C8E:C10	2.94	0.45
3:A:803:C8E:H22	3:A:805:C8E:H142	1.98	0.45
1:A:362:ASN:HD22	1:A:364:GLN:H	1.59	0.45
1:A:436:TYR:O	3:A:804:C8E:H202	2.17	0.45
1:A:372:GLN:NE2	4:A:809:HOH:O	2.49	0.45
1:A:426:THR:HG23	1:A:431:TRP:NE1	2.32	0.44
1:A:160:LEU:HD13	1:A:160:LEU:HA	1.60	0.44
1:A:146:SER:O	1:A:147:ASN:CB	2.62	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:803:C8E:H71	3:A:803:C8E:H101	1.25	0.44
1:A:369:GLY:HA3	3:A:800:C8E:C11	2.48	0.44
3:A:804:C8E:H82	3:A:804:C8E:H112	1.21	0.44
1:A:488:ASN:HB3	1:A:491:THR:CG2	2.47	0.44
1:A:169:LEU:O	1:A:169:LEU:HD12	2.18	0.43
1:A:162:ASP:C	1:A:163:LYS:CG	2.86	0.43
3:A:803:C8E:H172	3:A:803:C8E:H142	1.44	0.43
3:A:801:C8E:H142	4:A:861:HOH:O	2.18	0.43
1:A:164:THR:OG1	1:A:208:HIS:CD2	2.72	0.43
1:A:245:LEU:C	1:A:245:LEU:HD22	2.40	0.43
1:A:308:HIS:HB3	1:A:347:GLN:HE21	1.83	0.43
3:A:805:C8E:H161	3:A:805:C8E:H191	1.76	0.43
1:A:555:VAL:HG12	1:A:556:THR:HG23	2.02	0.42
3:A:805:C8E:H52	3:A:806:C8E:H41	2.01	0.42
1:A:526:ARG:C	1:A:527:TYR:HD1	2.23	0.42
1:A:245:LEU:HD22	1:A:246:TYR:N	2.34	0.42
1:A:160:LEU:CD2	1:A:166:VAL:CG2	2.95	0.42
1:A:157:GLN:C	1:A:158:GLN:HG2	2.40	0.42
1:A:462:LYS:HB3	3:A:804:C8E:H201	2.02	0.42
1:A:174:HIS:HB2	1:A:198:LEU:CD2	2.49	0.42
3:A:801:C8E:H131	3:A:801:C8E:H102	1.44	0.41
1:A:84:ARG:HH11	1:A:318:GLN:HE22	1.67	0.41
1:A:488:ASN:CB	1:A:491:THR:HG22	2.50	0.41
1:A:491:THR:OG1	1:A:493:THR:HG23	2.20	0.41
1:A:163:LYS:HB3	1:A:209:ASN:O	2.21	0.41
1:A:330:GLU:HG3	1:A:330:GLU:H	1.55	0.41
3:A:800:C8E:H112	3:A:800:C8E:H141	1.07	0.40
1:A:31:ARG:O	1:A:31:ARG:HD3	2.21	0.40
1:A:291:ASP:HA	1:A:326:THR:HG23	2.03	0.40
1:A:142:ALA:HB1	1:A:151:ASN:O	2.21	0.40
1:A:407:ASN:HD22	1:A:408:PRO:N	2.18	0.40
3:A:801:C8E:H141	3:A:801:C8E:H171	1.73	0.40
1:A:411:ASP:N	1:A:455:ASN:HD21	2.00	0.40
1:A:594:PHE:N	1:A:594:PHE:CD1	2.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	541/594 (91%)	522 (96%)	15 (3%)	4 (1%)	26 19

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	147	ASN
1	A	456	GLU
1	A	513	ASP
1	A	121	ASP

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	457/495 (92%)	415 (91%)	42 (9%)	11 6

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	13	ASN
1	A	21	THR
1	A	31	ARG
1	A	47	ARG
1	A	60	SER
1	A	103	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	138	THR
1	A	144	TRP
1	A	155	SER
1	A	158	GLN
1	A	160	LEU
1	A	162	ASP
1	A	163	LYS
1	A	169	LEU
1	A	174	HIS
1	A	198	LEU
1	A	206	LEU
1	A	215	SER
1	A	245	LEU
1	A	260	LEU
1	A	262	LYS
1	A	265	LEU
1	A	266	ILE
1	A	330	GLU
1	A	345	LEU
1	A	346	GLN
1	A	348	VAL
1	A	404	PHE
1	A	407	ASN
1	A	423	GLU
1	A	425	LEU
1	A	426	THR
1	A	510	GLN
1	A	511	LEU
1	A	519	THR
1	A	539	VAL
1	A	551	VAL
1	A	559	LEU
1	A	564	LYS
1	A	589	SER
1	A	594	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	98	GLN
1	A	147	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	150	GLN
1	A	157	GLN
1	A	159	GLN
1	A	174	HIS
1	A	176	HIS
1	A	208	HIS
1	A	225	ASN
1	A	248	GLN
1	A	295	GLN
1	A	302	ASN
1	A	318	GLN
1	A	320	GLN
1	A	337	ASN
1	A	347	GLN
1	A	362	ASN
1	A	372	GLN
1	A	400	GLN
1	A	407	ASN
1	A	455	ASN
1	A	506	GLN
1	A	510	GLN
1	A	521	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	C8E	A	800	-	20,20,20	0.54	0	19,19,19	1.04	2 (10%)
3	C8E	A	801	-	20,20,20	0.59	0	19,19,19	0.88	1 (5%)
3	C8E	A	802	-	20,20,20	0.40	0	19,19,19	0.76	0
3	C8E	A	803	-	20,20,20	0.38	0	19,19,19	0.49	0
3	C8E	A	804	-	20,20,20	0.40	0	19,19,19	0.75	0
3	C8E	A	805	-	20,20,20	0.56	0	19,19,19	0.45	0
3	C8E	A	806	-	20,20,20	0.56	0	19,19,19	0.48	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	C8E	A	800	-	-	0/18/18/18	0/0/0/0
3	C8E	A	801	-	-	0/18/18/18	0/0/0/0
3	C8E	A	802	-	-	0/18/18/18	0/0/0/0
3	C8E	A	803	-	-	0/18/18/18	0/0/0/0
3	C8E	A	804	-	-	0/18/18/18	0/0/0/0
3	C8E	A	805	-	-	0/18/18/18	0/0/0/0
3	C8E	A	806	-	-	0/18/18/18	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	800	C8E	O12-C11-C10	-2.25	100.38	110.36
3	A	800	C8E	O9-C8-C7	-2.23	100.92	109.87
3	A	801	C8E	C6-C7-C8	-2.02	104.45	113.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	800	C8E	6	0
3	A	801	C8E	3	0
3	A	802	C8E	7	0
3	A	803	C8E	12	0
3	A	804	C8E	4	0
3	A	805	C8E	12	0
3	A	806	C8E	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	549/594 (92%)	0.06	33 (6%) 25 27	28, 40, 67, 97	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	328	TYR	6.0
1	A	162	ASP	5.9
1	A	6	ASP	5.7
1	A	277	TYR	5.7
1	A	594	PHE	5.5
1	A	177	GLY	5.4
1	A	144	TRP	5.3
1	A	512	TYR	4.7
1	A	288	ALA	4.1
1	A	592	TYR	3.8
1	A	241	ASP	3.7
1	A	448	ASP	3.1
1	A	404	PHE	3.1
1	A	330	GLU	3.0
1	A	324	PRO	2.9
1	A	242	THR	2.9
1	A	135	GLU	2.8
1	A	331	ASP	2.8
1	A	531	TYR	2.8
1	A	160	LEU	2.7
1	A	134	ASP	2.6
1	A	176	HIS	2.5
1	A	451	LEU	2.5
1	A	449	HIS	2.4
1	A	148	SER	2.4
1	A	161	GLY	2.4
1	A	332	GLY	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	454	TYR	2.4
1	A	137	GLY	2.4
1	A	580	GLN	2.3
1	A	558	HIS	2.2
1	A	289	THR	2.2
1	A	511	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	C8E	A	806	21/21	0.46	0.36	8.56	49,100,128,136	0
3	C8E	A	801	21/21	0.90	0.20	6.34	47,68,107,111	0
3	C8E	A	805	21/21	0.76	0.17	2.96	61,79,107,109	0
3	C8E	A	800	21/21	0.82	0.20	2.66	42,58,84,96	0
3	C8E	A	803	21/21	0.85	0.19	2.53	49,89,110,117	0
3	C8E	A	802	21/21	0.92	0.20	2.43	38,57,77,86	0
3	C8E	A	804	21/21	0.86	0.17	1.66	39,58,86,102	0
2	MG	A	595	1/1	0.87	0.05	-	48,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.